

## SEARCH REQUEST FORM

58344

Requestor's

Name:

Natalia Davis

Serial

Number:

09/674436

Date:

1-14-02

Phone:

308-6410

Art Unit:

1642

Mailbox 8512

MSG

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Please search SEQ ID NO: 1 and for  
the gene "Any-RF" which may be derived  
from *Antheraea yamamai* OR a  
dormancy-control substance, which  
prevents insects from going into  
dormancy in the fall.

SEQ ID NO: = Asp-Ile-Leu-Arg-Gly

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## STAFF USE ONLY

Date completed: 1/23

Searcher:

D. S. L. 308-4292

Search Site

STIC

Vendors

IG Suite

Terminal time:

21

CM-1

12014

STN 5245

Elapsed time:

11

Pre-S

Dialog

CPU time:

Type of Search

APS

Total time:

N.A. Sequence

Geninfo

Number of Searches:

A.A. Sequence

SDC

Number of Databases:

7

Structure

DARC/Questel

Bibliographic

Other

Compugen



=> fil hcaplus  
FILE 'HCAPLUS' ENTERED AT 15:48:09 ON 23 JAN 2002  
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.  
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
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FILE COVERS 1907 - 23 Jan 2002 VOL 136 ISS 4  
FILE LAST UPDATED: 21 Jan 2002 (20020121/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

This file supports REGISTRY for direct browsing and searching of all substance data from the REGISTRY file. Enter HELP FIRST for more information.

HCAplus now provides online access to patents and literature covered in CA from 1907 to the present. Bibliographic information and abstracts were added in 2001 for over 3.8 million records from 1907-1966.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (742 field) in this file.

= d que 17

L1 210 SEA FILE=REGISTRY DILRG/SQSP  
L1 153 SEA FILE=HCAPLUS L1  
L1 300 SEA FILE=HCAPLUS ANTHEREA OR ANTHERAEA  
L4 111 SEA FILE=HCAPLUS YAMAMAI  
L5 9212 SEA FILE=HCAPLUS DORMANT OR DORMANCY  
L6 47404 SEA FILE=HCAPLUS LARVA?  
L7 2 SEA FILE=HCAPLUS L2 AND ((L3 OR L4 OR L5 OR L6))

= d bin abs 17 1-2

L ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2002 ACS  
AN 2 00:522576 HCAPLUS  
DI 133:131471  
TI Silkworm diapause regulatory gene Any-8F and method of isolation of its protein product  
IN Kotaki, Toyomi; Tsukada, Masuhiro; Sasaki, Koichi; Yang, Ping  
PA Norin Suisansho Sanshi Konchu Nogyo Gijyutsu Kenkyusho, Japan  
SO Jpn. Tokkyo Koho, 12 pp.  
CITEH: TEXT  
DT Patent  
LA Japanese  
FAN CNT 2  

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2000-42254	A1	20001212	1-100-1999	19990431

Search completed by David Schreiber Davis 09/6/04, 436



WO 2000073441 A1 20001207 WO 2000-JP3388 20000526  
W: CA, US  
RW: DE, FR, GB  
EP 1101119 A1 20010513 EP 2000-331578 20000526  
E: DE, FR, GB, SI, LT, LV, RO  
PRAI JP 1999-152273 A 19990531  
JP 2000-81012 A 20000312  
WO 2000-JP3388 W 20000516

AB Silkworm Any-BF gene involved in diapause regulation, and method of isolation of its protein product, are disclosed. A protein isolated from silkworm *Antheraea yamamai* using RP-HPLC and ion exchange HPLC and its C-terminally amidated peptide fragment demonstrated diapause regulatory activity.

L7 ANCHER 2 OF 2 NCAPLUS COPYRIGHT 2002 ACS

AN Ident: 10151 NCAPLUS

DE Ident: 10151

TI A putative juvenile hormone-binding protein from *larvae* of *Manduca sexta*: a putative receptor for the metamorphic action of juvenile hormone

AU Palli, Subba R.; Touhara, Kazushige; Charles, Jean-Philippe; Bonning, Bryony C.; Atkinson, Jeffrey K.; Trowell, Stephen C.; Hiruma, Kiyoshi; Goodman, Walter G.; Kyriakides, Themis; et al.

CS Dep. Zoology, Univ. Washington, Seattle, WA, 98195, USA

SO Proc. Natl. Acad. Sci. U. S. A. (1994), 91(13), 6191-5

CODEN: PNASAG; ISSN: 0027-8124

DT Journal

LA English

AB A 1.1-kb nuclear juvenile hormone (JH)-binding protein from the epidermis of *Manduca sexta* *larvae* was purified by using the photoaffinity analog for JH II ([3H]epoxyhomofarnesyl diazoacetate) and partially sequenced. A 1.1-kb cDNA was isolated by using degenerate oligonucleotide primers for PCR based on these sequences. The cDNA encoded a 262-amino acid protein that showed no similarity with other known proteins, except for short stretches of the interphotoreceptor retinoid-binding protein, rhodopsin, and human nuclear protein p68. Recombinant baculovirus contg. this cDNA made a 29-kDa protein that was covalently modified by [3H]epoxyhomofarnesyl diazoacetate and specifically bound the natural enantiomer of JH I ( $K_d = 10.7$  nM). This binding was inhibited by the natural JHs but not by methoprene. Immunocytochem. anal. showed localization of this 29-kDa protein to epidermal nuclei. Both mRNA and protein are present during the intermolt periods; during the *larval* molt, the mRNA disappears but the protein persists. Later when cells become pupally committed, both the mRNA and protein disappear with a transient reappearance near pupal ecdysis. The properties of this protein are consistent with its being the receptor necessary for the ant metamorphic effect of JH.

=> fil.kem

FILE 'HOME' ENTERED AT 15:48:59 ON 23 JAN 2002



09/674436

L1 FILE 'REGISTRY' ENTERED AT 10:59:43 ON 23 JAN 2002  
210 S DILRG/SQSP

L2 FILE 'CAPLUS' ENTERED AT 11:00:05 ON 23 JAN 2002  
155 S L1

L4 3 S L2 AND RF  
L5 2 S L2 AND DIAPAUSE  
L6 4 S L4 OR L5

L6 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:364016 CAPLUS

DOCUMENT NUMBER: 135:1093

TITLE: The malaria genome sequencing project: Complete sequence of Plasmodium falciparum chromosome 2

AUTHOR(S): Gardner, M. J.; Tettelin, H.; Carucci, D. J.; Cummings, L. M.; Smith, H. O.; Fraser, C. M.; Venter, J. C.; Hoffman, S. L.

CORPORATE SOURCE: The Institute for Genomic Research, Rockville, MD, 20850, USA

SOURCE: Parassitologia (Roma, Italy) (1999), 41(1-3), 69-75

CODEN: PSSGAR; ISSN: 0048-2951

PUBLISHER: Lambardo Editore

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An international consortium has been formed to sequence the entire genome of the human malaria parasite Plasmodium falciparum. Chromosome 2 of clone 3D7 was sequenced using a shotgun sequencing strategy. Chromosome 2 is 947 kb in length, has a base compn. of 80.2% A+T, and contains 210 predicted genes. In comparison to the Saccharomyces cerevisiae genome, chromosome 2 has a lower gene d., a greater proportion of genes contg. introns, and nearly twice as many proteins contg. predicted non-globular domains. A group of putative surface proteins was identified, rifins, which are encoded by a gene family comprising up to 7% of the protein-encoding genes in the genome. The rifins exhibit considerable sequence diversity and may play an important role in antigenic variation. Sixteen genes encoded on chromosome 2 showed signs of a plastid or mitochondrial origin, including several genes involved in fatty acid biosynthesis. Completion of the chromosome 2 sequence demonstrated that the A+T-rich genome of P. falciparum can be sequenced by the shotgun approach. Within 2-3 yr, the sequence of almost all P. falciparum genes will have been detd., paving the way for genetic, biochem. and immunol. research aimed at developing new drugs and vaccines against malaria.

IT 257896-56-3

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; complete sequence of Plasmodium falciparum chromosome 2)

REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2000:772766 CAPLUS

DOCUMENT NUMBER: 133:330556





09/674436

TITLE: Genome sequence and polypeptides of *Pyrococcus abyssi* and their uses  
INVENTOR(S): Forterre, Patrick; Thierry, Jean-Claude; Prieur, Daniel; Dietrich, Jacques; Lecompte, Odile; Querellou, Joel; Weissenbach, Jean; Saurin, William; Heilig, Roland; Flament, Didier; Raffin, Jean-Paul; Henneke, Ghislaine; Gueguen, Yannick; Rolland, Jean-Luc  
PATENT ASSIGNEE(S): Centre National de la Recherche Scientifique (CNRS), Fr.; Institut Francais de Recherche pour l'Exploitation de la Mer - IFREMER  
SOURCE: PCT Int. Appl., 1403 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: French  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000065062	A2	20001102	WO 2000-FR1065	20000421
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
FR 2792651	A1	20001027	FR 1999-5034	19990421

PRIORITY APPLN. INFO.: FR 1999-5034 A 19990421

AB The invention relates to the genome sequence of *Pyrococcus abyssi* strain Orsay, the 807 open reading frame nucleotide sequences coding for polypeptides of *P. abyssi* such as polypeptides involved in metab. or in the replication process, in addn. to vectors including said sequences and cells transformed by said vectors. Replication factor C (large and small forms resulting from intein splicing), PCNA (proliferating cell nuclear antigen), DNA polymerase II large and small subunits, replication factor A, and DNA polymerase I were isolated and characterized by recombinant cloning in *Escherichia coli*. The invention also relates to methods using said nucleic acids or polypeptides, esp. biosynthesis methods or biodegrdn. methods for mols. of interest and to kits comprising said polypeptides.

IT 302870-69-5

RL: BOC (Biological occurrence); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)  
(amino acid sequence; genome sequence and polypeptides of *Pyrococcus abyssi* and their uses)

L6 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2000:522576 CAPLUS

DOCUMENT NUMBER: 133:131471

TITLE: Silkworm **diapause** regulatory gene Any-  
**RF** and method of isolation of its  
protein product

Searcher : Shears 308-4994



09/674436

INVENTOR(S): Kotaki, Toyomi; Tsukada, Masuhiro; Suzuki,  
Koichi; Yang, Ping  
PATENT ASSIGNEE(S): Norin Suisansho Sanshi Konchu Nogyo Gijutsu  
Kenkyusho, Japan  
SOURCE: Jpn. Tokkyo Koho, 12 pp.  
CODEN: JTXFFF  
DOCUMENT TYPE: Patent  
LANGUAGE: Japanese  
FAMILY ACC. NUM. COUNT: 2  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 3023790	B1	20000321	JP 1999-152273	19990531
JP 2000342254	A2	20001212		
WO 2000073441	A1	20001207	WO 2000-JP3388	20000526
W: CA, US RW: DE, FR, GB				
EP 1101819	A1	20010523	EP 2000-931578	20000526
R: DE, FR, GB, SI, LT, LV, RO				
PRIORITY APPLN. INFO.:			JP 1999-152273	A 19990531
			JP 2000-81012	A 20000322
			WO 2000-JP3388	W 20000526

AB Silkworm Any-**RF** gene involved in **diapause** regulation, and method of isolation of its protein product, are disclosed. A protein isolated from silkworm *Antheraea yamamai* using RP-HPLC and ion exchange HPLC and its C-terminally amidated peptide fragment demonstrated **diapause** regulatory activity.

IT **286408-63-7**  
RL: BOC (Biological occurrence); BPR (Biological process); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PROC (Process)  
(amino acid sequence; silkworm **diapause** regulatory gene  
Any-**RF** and method of isolation of protein product)

L6 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1998:505667 CAPLUS

DOCUMENT NUMBER: 129:229492

TITLE: Cloning of leukemia inhibitory factor (LIF) and its expression in the uterus during embryonic **diapause** and implantation in the mink (*Mustela vison*)

AUTHOR(S): Song, Jian H.; Houde, Alain; Murphy, Bruce D.  
CORPORATE SOURCE: Cent. Recherche Reproduction Animale, Fac. Med. Veterinaire, Univ. Montreal, St-Hyacinthe, PQ, J2S 7C6, Can.

SOURCE: Mol. Reprod. Dev. (1998), 51(1), 13-21  
CODEN: MREDEE; ISSN: 1040-452X

PUBLISHER: Wiley-Liss, Inc.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Leukemia inhibitory factor (LIF) is essential for embryo implantation in mice. Whether LIF plays a role in termination of embryonic **diapause** and initiation of implantation in carnivores, esp. in species with obligate delayed implantation such as the mink, is not known. The objectives of this study were to clone the LIF coding sequence in the mink and det. its mRNA abundance in the uterus through embryonic **diapause**,

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implantation, and early postimplantation. The authors show that the mink LIF cDNA contains 609 nt encoding a deduced protein of 203 amino acids. The homologies are 80.6, 90, 88.2, 87.6, and 86.8% in coding sequence and 79.2, 90.1, 91, 90.1 and 85.4% in amino acid sequence with mouse, human, pig, cow, and sheep resp. Glycosylation sites and disulfide bonds present in other species are generally conserved in the mink LIF sequence. Quantitation by polymerase chain reaction amplification indicates that LIF mRNA is expressed in mink uterus just prior to implantation and during the first two days after implantation, but not during **diapause** or later after implantation pregnancy. The abundance of LIF mRNA was significantly higher in the uterus at the embryo expansion stage than at days 1-2 of postimplantation. By immunohistochem. localization it was shown that LIF is expressed in the uterine epithelial glands at time of embryonic expansion and in early postimplantation. The coincidence of LIF expression with implantation in this species suggests that LIF is involved in the implantation process, and may be a maternal signal which terminates obligate embryonic **diapause**.

IT 212846-19-0

RL: PRP (Properties)

(amino acid sequence; cloning of leukemia inhibitory factor (LIF) and expression in uterus during embryonic **diapause** and implantation in mink (*Mustela vison*))

E1 THROUGH E4 ASSIGNED

~~FILE~~ 'REGISTRY' ENTERED AT 11:03:47 ON 23 JAN 2002

L7 4 SEA FILE=REGISTRY ABB=ON PLU=ON (212846-19-0/BI OR 257896-56-3/BI OR 286408-63-7/BI OR 302870-69-5/BI)

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L8 4 L7 AND L1

L8 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2002 ACS

RN 302870-69-5 REGISTRY

CN Protein ORF 756 (*Pyrococcus abyssi* strain Orsay) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 457: PN: W00065062 SEQID: 756 claimed protein

CI MAN

SQL 310

SEQ 1 MVVSMREGEI ISLFMKHFER HSLGDDAGFI KLNNSWLLVT SDMLVWKTDV  
51 PDFMTPEDAG RKVVTMNVSD IAAMGGRPMA FFFSLAVPGD VSEDILRGIA

=====

101 RGINEGSKVY KLIKIVSGDTN EADDIIIDGG SLGIGKRLLL RSNAPGDLV  
151 CVTGDLGRPL TALLLWMRGE KIPREIEEKA RNPRARVEEG VKLSSLANSA  
201 IDISDGLSKE LWEIANASNV RIIIEEERLP ISDSVKEIVS DPVKVALASG  
251 EEFEELLFTIP REKVEELDID FKIIIGRVEGG NGVYIKRGRK IEELEVLGWE  
301 HLAGGIDVEL

HITS AT: 94-98

REFERENCE 1: 133:330556

L8 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2002 ACS

RN 286408-63-7 REGISTRY

CN Glycine, L-.alpha.-aspartyl-L-isoleucyl-L-leucyl-L-arginyl- (9CI)  
(CA INDEX NAME)

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09/674436

OTHER NAMES:

CN 1: PN: JP3023790 PAGE: 9 claimed sequence  
CN Protein gene Any-RF (Antheraea yamamai fragment)  
SQL 5

SEQ 1 DILRG  
=====

HITS AT: 1-5

REFERENCE 1: 133:131471

L8 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2002 ACS  
RN 257896-56-3 REGISTRY  
CN Phosphatase (acid phosphatase family) (Plasmodium falciparum gene PFB0380c) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 5: PN: WO0025728 SEQID: 75 claimed protein  
CN GenBank AE001391-derived protein GI 3845169  
CN Phosphatase, acid (Plasmodium falciparum clone 3D7 gene PFB0380c)  
CN Protein (Plasmodium falciparum clone p3D7 chromosome 2 gene PFB0380)  
CI MAN  
SQL 2010

SEQ 1 MLIKQEPKEV EKKEEKEKKG AKDKGKDLFS LNKKRERKKK ESQKIDRYLI  
51 NSCDSNKSNY SCCYLNNECF VKNISICKKC MFSYFEFKNV TKVIYMRHGA  
101 RTPKKKIKNI WPFKEGKGD L TFLGFQQSIK VGEYLRKYYY TFNKLNKKYN  
151 KRERGLRINN KEKGYIKKNK CDVKKCKTLY KNKYNNNNNN NNNHYVINEK  
201 YNGSNKNDYV KNNTYDNKG Y SYLYDLSTSF NELENRRKRL HKFPYLRDFI  
251 YYEKYFLKIN KRSNKHQRKV FIKIKRRRRN NILKIWIHQH LINKMKKIKN  
301 KNMNNYNKCY IKFSSIRKRG YHKMENIECN NKNNDDDDND DNNHNNNDND  
351 NNNNNDDNNN DDNNNDNNNN NDDNNNNND DDNNYYYYNY NNDETPFNNK  
401 SFNYADMLKY TKYYYKNILK DKKNYITNNK KKELFFPLME HLYMYKKKL  
451 INKMKEKNIK KKKKKYDKII KLINKYLCIK TTNSECKLT AYGIICGILG  
501 ISEYIYFFFF ILFFKSNDYK TNDNNIDTYT KRKEKKKCLN KRSKCFQNW  
551 LNRDITSGQY NCIDKNTAPV KNYIIGENLC GENGCGKNGC GDILRGDILC  
=====  
601 GDILRGDNNS IPLFRSNRIF CKQSKITFCD ELYIYFNKIL KRLQSLDDMY  
=====  
651 KINHEVKMFG NDKDVLNNSY KKC YDKNDYG SYPSYNKYSN DYKSHYVIK  
701 MKNVKSQVCS NESIILKERQ ENEKKKKKKK KMENTFINN NNI MYNINVF  
751 FDLIINERGN FQFFYNNIK KRQNEKGLE EWNVYNIFQL YMKYILNEFS  
801 KFFKLKFLN KNVENIDNTF NSITNIYNKY YINMVVHRKD CFEKKQIHSK  
851 EHMMKKIHLR DKFIEYEKEN EIIDNCNNIN MDNKKKEINN NYNNMIDNN  
901 IEIDMSNNFI FTYYYIFYLL NYMDTYIQFL FYLLKNTYIL FSVVKVAERN  
951 SLMLKTLTK NHYIKLRNH IHNSDVYKI LNNYKDEIF IVYDITKWE  
1001 NCMNTTDILY NDVKKNTKID DLENIDIPII TNDKEEYHVN NSIISVLKKH  
1051 NSSVYKLKKK LKNSIILKDL KKLNCNFINK NYIHNTNYDK HNKIYQDKIK  
1101 NWTYHPFHNK KKNVKIIFK ISAYDAYIYH GVNLLNLFNR AYEKLSQHPP  
1151 SSIDLIKKEY GQNNYIINCE IKKYEEQNNF IIKRPNINIS GKNLSCHNKT  
1201 NSSNTLQGNF EKANILADE RRLKRKNKI QNRKVVQNGM TINNSKKYR  
1251 NNQTEYYEKK EKKKKYDQKN DQTNEQKCAQ KNDQTNEQKN DQTDNDQNDQ  
1301 TNDQTKIRF YKNIYTCYKL MCKNEYSNKY LSWLCSGMSL  
1351 IDVVINFIIN VELYEKYNKE NKTTKCFIPR IILYLTHQSS ILSFQSCVGI  
1401 RKKDMKIPPF ASFISLELIH IKKKKIKNLS NKLCNVSNNE KSYCYSNKYN  
1451 IMKGEKKKHA SSRSVHVNT DRTDVLFSFIY HNNTANIFCC KDDCVWKVRE  
1501 TENEKKFEK EKNKKFMNEE NENVIKDDEK NIYNILKRN NENIDKKKSI  
1551 NINTCIYNDI PTNVNNKKYE SYLPKCLNKI HDFKNLFYLL CYKNNNIQDL  
1601 IQLYDICLNN NYTHIKKNMQ LKEGKKHGKR NFYGYFVKFT FNSVPLKLL

The first part of the paper discusses the importance of understanding the cultural context of the research. It highlights the need for researchers to be sensitive to the values and beliefs of the communities they are studying. This is particularly important in the field of health research, where cultural differences can significantly impact the effectiveness of interventions.

The second part of the paper presents a case study of a health intervention in a rural community. The study found that the intervention was more successful when it was tailored to the local culture and beliefs. This suggests that a one-size-fits-all approach is not always the best solution.

The third part of the paper discusses the challenges of conducting research in a culturally diverse environment. It notes that researchers often face difficulties in finding a common ground between their own cultural assumptions and those of the community being studied.

The fourth part of the paper offers some suggestions for how to overcome these challenges. It suggests that researchers should engage in a process of cultural learning and reflection. This involves taking the time to understand the community's perspective and being open to the possibility that one's own assumptions may be flawed.

The fifth part of the paper concludes by emphasizing the importance of cultural competence in research. It argues that researchers who are culturally competent are better equipped to design and implement effective interventions.



09/674436

1651 KNKLIKKNYM GNKKDKKEEDN NYHNDKNNYS DNIFYDNHDT NNNNNNNNNN  
1701 NNNSNNNNNN NICLKNNKNN IMHEDINANK RESLKKKKKK KKKNCIQKNN  
1751 NICERKKSNI HNNSSKYIFN TVRFFKMMDI AKINTNKKCD ENSISCINNM  
1801 REKRNIKKNL NRNILNFNNS NNDKYMNYIY NSTNVTYGKN YKRINKKDVH  
1851 INNILLHTYK QHKKKKSTII SSDNNNNNNN NAEDDISSRK LKFKDIKGNT  
1901 KQKYINDHNN INSYDNNINN GLINEHKNVL HNECKNKNQ IIGYSIKYDK  
1951 NVVSENSCSD VITSLKDKKI KKRKKKLQKK NYENENIVCL DCLISYLKKM  
2001 LRIYGNPEIL

HITS AT: 592-596, 602-606

REFERENCE 1: 135:1093

REFERENCE 2: 132:330627

REFERENCE 3: 132:147372

L8 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2002 ACS

RN **212846-19-0** REGISTRY

CN Leukemia inhibitory factor (Mustela vison gene LIF) (9CI) (CA INDEX  
NAME)

OTHER NAMES:

CN GenBank AF048827-derived protein GI 2959710

CI MAN

SQL 202

SEQ 1 MKVLAAGVVP LLLVLHWKHG AGTPLPITPV NATCATRHPC HSNLMNQIRN  
51 QLAHVNGSAN ALFILYYTAQ GEPFPNNLDK LCGPNVTDFP PFHRNGTEKT  
101 RLVELYRIIA YLGASLGnit RDQKVLNPNALSLHSLKAT ADILRGLLSN  
=====

151 VLCRLCNKYH VAHVDVAYGP DTSGKDVQK KKLGCQLLGK YKQVIAVVAQ

201 AF

HITS AT: 142-146

REFERENCE 1: 129:229492

FILE 'HOME' ENTERED AT 11:04:12 ON 23 JAN 2002

11/11/11

11/11/11

11/11/11





RESULT 7  
US-09-602 640-1848  
Sequence 34921, Application 62/05811046-1  
GENERAL INFORMATION:  
APPLICANT: Goldmine, Betty S.  
APPLICANT: Shaker, Gregory J.  
APPLICANT: Wladimir, Robert C.  
TITLE OF INVENTION: Myocardial infarction and stroke prevention and uses thereof  
FILE REFERENCE: 48-1015449B  
CURRENT FILING DATE: 2001-07-10  
PRIOR FILING DATE: 2001-07-10  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 10425  
SEQ ID NO: 10453  
TYPE: 061  
ORIGIN: 92  
US-09-602-640-1848

Query Match 100.00% Score 259.14 Length 92  
Post Local Similarity 100.00% Prod. No. 674-436-1  
Matches 52 Conserved 20 of Mismatches 32 Gaps 0

Q# 1 11164 5  
L# 57 01164 61

RESULT 8  
PRT-0501-09681 64921  
Sequence 34921, Application 62/05811046-1  
GENERAL INFORMATION:  
APPLICANT: Hyslop, Inc.  
TITLE OF INVENTION: NOVEL NOVELLING ALKYL AND ALKYL ETHERS  
FILE REFERENCE: 21-272-0047  
CURRENT APPLICATION NUMBER: PCT/05811046-1  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 2000-03-31  
PRIOR FILING DATE: 2000-03-31  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 69736  
SOFTWARE: custom  
SEQ ID NO: 84921  
LENGTH: 66  
TYPE: 061  
ORIGIN: 92  
PRT-0501-09681 64921

Query Match 100.00% Score 259.14 Length 92  
Post Local Similarity 100.00% Prod. No. 674-436-1  
Matches 52 Conserved 20 of Mismatches 32 Gaps 0

Q# 1 11164 5  
L# 57 01164 61

RESULT 9  
US-09-627 629-5728  
Sequence 54921, Application 62/05811046-1  
GENERAL INFORMATION:  
APPLICANT: George H. Shiner, Jr.  
APPLICANT: George H. Miller  
APPLICANT: Robert S. Hare  
APPLICANT: Karen J. Shuk  
TITLE OF INVENTION: STATISTICAL ANALYSIS OF DATA  
TITLE OF INVENTION: STATISTICAL ANALYSIS OF DATA

NUMBER OF SEQUENCE: 54921  
APPLICANT: George H. Shiner, Jr.  
APPLICANT: George H. Miller  
APPLICANT: Robert S. Hare  
APPLICANT: Karen J. Shuk  
TITLE OF INVENTION: STATISTICAL ANALYSIS OF DATA  
FILE REFERENCE: 21-272-0047  
CURRENT APPLICATION NUMBER: PCT/05811046-1  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 2000-03-31  
PRIOR FILING DATE: 2000-03-31  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 69736  
SOFTWARE: custom  
SEQ ID NO: 84921  
LENGTH: 66  
TYPE: 061  
ORIGIN: 92  
US-09-627-629-5728

Query Match 100.00% Score 259.14 Length 92  
Post Local Similarity 100.00% Prod. No. 674-436-1  
Matches 52 Conserved 20 of Mismatches 32 Gaps 0

Q# 1 11164 5  
L# 57 01164 61

RESULT 10  
US-09-611 629-5728  
Sequence 54921, Application 62/05811046-1  
GENERAL INFORMATION:  
APPLICANT: George H. Shiner, Jr.  
APPLICANT: George H. Miller  
APPLICANT: Robert S. Hare  
APPLICANT: Karen J. Shuk  
TITLE OF INVENTION: STATISTICAL ANALYSIS OF DATA  
FILE REFERENCE: 21-272-0047  
CURRENT APPLICATION NUMBER: PCT/05811046-1  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 2000-03-31  
PRIOR FILING DATE: 2000-03-31  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 69736  
SOFTWARE: custom  
SEQ ID NO: 84921  
LENGTH: 66  
TYPE: 061  
ORIGIN: 92  
US-09-611-629-5728





Wed Jan 23 07:27:23 2002

us-09-674-436-1.rapm

Page 6









[illegible][illegible]

Author's address: Department of Mathematics, University of Illinois at Chicago, Chicago, IL 60607-7143, U.S.A.  
E-mail: jay@math.uic.edu

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• **COPIES OF THE ZEPHYRUS**  
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• **THE PUBLISHED NEWSLETTER**

NUMBER OF STUDENTS  
IN EACH PRACTICE GROUP

Figure 1 illustrates the experimental setup. A participant is seated at a table, looking at a screen. On the screen, there is a starting point (a large circle) and a target (a small circle). The distance between these two points is labeled 'Distance'. The participant's hand is positioned at the starting point, labeled 'Hand'.

Figure 1 is a schematic representation of the experimental design. It shows a sequence of events: a subject is presented with a stimulus (a face), then a response is recorded (a button press), and finally, the subject is presented with a feedback stimulus (a face). The response is recorded by a computer system, and the feedback stimulus is presented by a video screen. The sequence is labeled with 'Stimulus', 'Response', and 'Feedback'.

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1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

```

FILE REFERENCE: 2750-1243P
CURRENT ATTORNEY'S NUMBER: 55607706/427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: later in version 3.1
SEQ ID NO: 9445
LENGTH: 550
TYPE: Pct
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..550
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..550
OTHER INFORMATION: Xaa is any amino acid
US-09-708-427 9445

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Query Match: 100.0% Score: 25.1941 Length: 550
Best Local Similarity: 100.0% Prod. No. 134000
Matches: 5 Conservative of Mismatches: 0 of 0 gaps

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QY 1 Dllk3 5

DB 287 Dllk3 291

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*RESULT 15
US-09-708-427-58841
: Sequence 58841, Application US/09708427
: GENERAL INFORMATION:
: APPLICANT: N. ALEXANDROV et al.
: TITLE OF INVENTION: SEQUENCE DETERMINED FOR THE PROTEIN AND CHARACTERIZATION OF THE PROTEIN
: FILE REFERENCE: 2750-1243P
: CURRENT ATTORNEY'S NUMBER: 55607706/427
: CURRENT FILING DATE: 2000-11-09
: NUMBER OF SEQ ID NOS: 85364
: SOFTWARE: Patent in version 3.1
: SEQ ID NO: 9445
: LENGTH: 550
: TYPE: Pct
: ORGANISM: Zoa may's subsp. may's
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..550
: OTHER INFORMATION: Xaa is any amino acid
: NAME/KEY: misc_feature
: LOCATION: 1..550
: OTHER INFORMATION: Xaa is any amino acid
US-09-708-427-58841

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Query Match: 100.0% Score: 25.1941 Length: 550
Best Local Similarity: 100.0% Prod. No. 134000
Matches: 5 Conservative of Mismatches: 0 of 0 gaps

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QY 1 Dllk3 5

DB 176 Dllk3 180

Search completed: January 22, 2002, 14:25:44  
Job Time: 183 sec













Wed Jan 23 07:27:22 2002

[illegible]

2000	March	1	♂	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	100
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14 99 d1114 100

RESULT 6

AAK52542

110 AAK52542 standard: protein: 14. AA

XX

AAK52541.1

XX

23 FEB 2001 (1481 00112)

XX

HolIcortol pyrolytic bait polypeptide

XX

HolIcortol pyrolytic bait polypeptide

XX

HolIcortol pyrolytic

XX

4020006722 AL

XX

09 NOV 2000

XX

14 APR 2000: 2000W: 1000000

XX

30 APR 1999: 0000001.66

XX

(HHR) HHR: 0000000.00

XX

1000000.00

XX

1000000.00

XX

A two hybrid system for identifying and isolating proteins that interact with a bait polypeptide

XX

Example 5: 1000000.00

XX

The present sequence is a bait polypeptide

XX

pyrolytic bait polypeptide

XX

The method is used to identify a polypeptide which is capable of interacting with the bait

XX

polypeptide. The two hybrid system is used to screen for polypeptides

XX

for antibacterial activity. It may be used to screen for primers of

XX

specific detection probes. The polypeptides are used as bait or host cells can

XX

be used as immunogens to produce monoclonal antibodies. The

XX

polynucleotides, polypeptides, and host cells are used to produce a

XX

modulated antibody can be used to produce a polypeptide

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

14 99 d1114 100

RESULT 6

AAK52542

110 AAK52542 standard: protein: 14. AA

XX

AAK52541.1

XX

23 FEB 2001 (1481 00112)

XX

HolIcortol pyrolytic bait polypeptide

XX

HolIcortol pyrolytic bait polypeptide

XX

HolIcortol pyrolytic

XX

4020006722 AL

XX

09 NOV 2000

XX

14 APR 2000: 2000W: 1000000

XX

30 APR 1999: 0000001.66

XX

(HHR) HHR: 0000000.00

XX

1000000.00

XX

1000000.00

XX

A two hybrid system for identifying and isolating proteins that interact with a bait polypeptide

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XX

The present sequence is a bait polypeptide

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specific detection probes. The polypeptides are used as bait or host cells can

XX

be used as immunogens to produce monoclonal antibodies. The

XX

polynucleotides, polypeptides, and host cells are used to produce a

XX

modulated antibody can be used to produce a polypeptide

XX

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XX  
SL Sequence 194 AA:

Query Match: 100.00% Seq ID: 100.00% (100.00%)  
 Best Local Similarity: 100.00% (100.00%)  
 Matches: 11 (100.00%) of 11 (100.00%)

07 1 Dukes  
 10 121 diff 125

#### RESULT 15

AAR75345  
 ID AAR75345 standard: 194 AA:

XX  
 AAR75345:

XX  
 13-DEC-1995 (first entry)

XX  
 10E Hybrid human cytokine IL12:

XX  
 Hybrid cytokine: tumor promotion assay

XX  
 Synthetic:

XX  
 Key: Location/Qualifiers

XX  
 MI: Miscellaneous 192

XX  
 W051093A:

XX  
 18 MAY 1995:

XX  
 07-NOV-1994: 0480 0272673:

XX  
 08-NOV-1994: 9408-0139101:

XX  
 (H01C) H01C11N5-N CANCER RES CENTER (H01C)

XX  
 1994-1995: 19411/25:

XX  
 N PDB: AAR75345:

XX  
 New hybrid cytokines with alpha helical regions from different

XX  
 sources - also DNA encoding them, vector and transfected cells

XX  
 useful e.g. for treating cancer, removed for brevity

XX  
 Claim 11: page 43-44: 52pp: English:

XX  
 The cytokine encoding genes for leukemia inhibitory factor (LIF),

XX  
 granulocyte colony stimulating factor (G-CSF), interleukin 6 (IL-6),

XX  
 interleukin 11 (IL-11), colony neurotrophic factor 1 (CNTF) and

XX  
 oncostatin M (OSM) have been cloned and inserted into the 1100 base

XX  
 1.2 kb LIF, G-CSF and OSM composite four alpha helical sequences. In

XX  
 each cytokine, the four alpha helices, separated by the fused LIF

XX  
 alpha helical "linker" sequences of about 100 bases, the linker

XX  
 provides a group of three separate hybrid cytokines, having a size similar

XX  
 to about 1000 bases. Each hybrid cytokine comprises three or

XX  
 four alpha helical sequences and linking sequences, resulting from about

XX  
 5-40 AAs in length. In the nomenclature of a hybrid cytokine, the

XX  
 upper case letters designate alpha helices, and lower case letters

XX  
 designate linker sequences. The first three alpha helical

XX  
 sequences of LIF were derived from LIF, and the fourth

XX  
 alpha sequence was derived from IL-11.

Best Local Similarity: 100.00% Seq ID: 100.00% (100.00%)

07 1 Dukes

10 121 diff 125

Search completed: 100.00% (100.00%)



Database version 1.5  
Copyright (c) 1994-2000 by the authors

db protein - protein search, using sw method

begin on: January 22, 2002 11:22:22 - End on: January 22, 2002 11:22:22

(No. of all proteins)  
720 - Multiple seq. updates/sec

Hitset:

Protein source:

Sequences:

Showing full set

Sort order:

Total number of hits satisfying chosen parameters: 21,247

Minimum job seq. length: 9

Maximum job seq. length: 20000000

Post processing: Minimum Match: 99

Maximum Match: 100  
Listed first 40 summaries

Database: 1 Issued Patterns: 40

1: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
2: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
3: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
4: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
5: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
6: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
7: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
8: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
9: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
10: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
11: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
12: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
13: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
14: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
15: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
16: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
17: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
18: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
19: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
20: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
21: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
22: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
23: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
24: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
25: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
26: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0  
27: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0

Prod. No. is the number of results produced by choice to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total set of hits.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	25	100.0	158	2	US-09-674-436-1	Sequence 1: AFI1
2	25	100.0	179	1	US-08-076-087	Sequence 1: AFI1
3	25	100.0	179	1	US-08-411-2-1	Sequence 1: AFI1
4	25	100.0	179	5	US-08-088-879-1	Sequence 1: AFI1
5	25	100.0	181	4	US-08-088-879-1	Sequence 1: AFI1
6	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
7	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
8	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
9	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
10	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
11	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
12	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
13	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
14	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
15	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
16	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
17	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
18	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
19	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
20	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
21	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
22	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
23	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
24	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
25	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
26	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1
27	25	100.0	181	6	US-08-088-879-1	Sequence 1: AFI1

# ALTERNATE

1	US-09-674-436-1	Sequence 1: AFI1
2	US-08-076-087	Sequence 1: AFI1
3	US-08-411-2-1	Sequence 1: AFI1
4	US-08-088-879-1	Sequence 1: AFI1
5	US-08-088-879-1	Sequence 1: AFI1
6	US-08-088-879-1	Sequence 1: AFI1
7	US-08-088-879-1	Sequence 1: AFI1
8	US-08-088-879-1	Sequence 1: AFI1
9	US-08-088-879-1	Sequence 1: AFI1
10	US-08-088-879-1	Sequence 1: AFI1
11	US-08-088-879-1	Sequence 1: AFI1
12	US-08-088-879-1	Sequence 1: AFI1
13	US-08-088-879-1	Sequence 1: AFI1
14	US-08-088-879-1	Sequence 1: AFI1
15	US-08-088-879-1	Sequence 1: AFI1
16	US-08-088-879-1	Sequence 1: AFI1
17	US-08-088-879-1	Sequence 1: AFI1
18	US-08-088-879-1	Sequence 1: AFI1
19	US-08-088-879-1	Sequence 1: AFI1
20	US-08-088-879-1	Sequence 1: AFI1
21	US-08-088-879-1	Sequence 1: AFI1
22	US-08-088-879-1	Sequence 1: AFI1
23	US-08-088-879-1	Sequence 1: AFI1
24	US-08-088-879-1	Sequence 1: AFI1
25	US-08-088-879-1	Sequence 1: AFI1
26	US-08-088-879-1	Sequence 1: AFI1
27	US-08-088-879-1	Sequence 1: AFI1

1. PERSONAL INFORMATION  
 a. NAME: [REDACTED]  
 b. ADDRESS: [REDACTED]  
 c. PHONE: [REDACTED]  
 d. DATE OF BIRTH: [REDACTED]  
 e. SEX: [REDACTED]  
 f. RACE: [REDACTED]  
 g. RELIGION: [REDACTED]  
 h. OCCUPATION: [REDACTED]  
 i. EDUCATION: [REDACTED]  
 j. MARITAL STATUS: [REDACTED]  
 k. CHILDREN: [REDACTED]  
 l. PARENTS: [REDACTED]  
 m. SIBLINGS: [REDACTED]  
 n. ANCESTRY: [REDACTED]  
 o. OTHER: [REDACTED]

2. EDUCATION  
 a. SCHOOL: [REDACTED]  
 b. DEGREE: [REDACTED]  
 c. MAJOR: [REDACTED]  
 d. MINOR: [REDACTED]  
 e. INSTITUTION: [REDACTED]  
 f. LOCATION: [REDACTED]  
 g. DATES: [REDACTED]  
 h. FACULTY: [REDACTED]  
 i. STUDENTS: [REDACTED]  
 j. ADVISORS: [REDACTED]  
 k. OTHER: [REDACTED]

3. EMPLOYMENT  
 a. EMPLOYER: [REDACTED]  
 b. POSITION: [REDACTED]  
 c. DATES: [REDACTED]  
 d. LOCATION: [REDACTED]  
 e. INDUSTRY: [REDACTED]  
 f. DEPARTMENT: [REDACTED]  
 g. DIVISION: [REDACTED]  
 h. TEAM: [REDACTED]  
 i. PROJECTS: [REDACTED]  
 j. ACHIEVEMENTS: [REDACTED]  
 k. OTHER: [REDACTED]

4. TRAVEL  
 a. COUNTRY: [REDACTED]  
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 c. STATE: [REDACTED]  
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 e. DATES: [REDACTED]  
 f. PURPOSE: [REDACTED]  
 g. ACCOMMODATIONS: [REDACTED]  
 h. TRANSPORTATION: [REDACTED]  
 i. OTHER: [REDACTED]

5. REFERENCES  
 a. NAME: [REDACTED]  
 b. ADDRESS: [REDACTED]  
 c. PHONE: [REDACTED]  
 d. RELATIONSHIP: [REDACTED]  
 e. DATES: [REDACTED]  
 f. OTHER: [REDACTED]

6. NOTES  
 a. [REDACTED]  
 b. [REDACTED]  
 c. [REDACTED]  
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 e. [REDACTED]  
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 x. [REDACTED]  
 y. [REDACTED]  
 z. [REDACTED]

Page 3

APPELLANI, A. V. 1953. *Methods and Materials of Field Ornithology*. John Wiley & Sons, New York.

NUMBER OF SEQUENCES: 11  
 -[JOURNAL] ADDRESS: N/A  
 ADDRESS: N/A  
 ADDRESS: N/A

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INTRODUCTION  
MATERIALS AND METHODS  
RESULTS  
DISCUSSION  
CONCLUSIONS  
REFERENCES

1	TRAINING SET DATA	94.0
2	APPROXIMATION ERROR	94.0
3	VALIDATION SET DATA	94.2
4	APPROXIMATION ERROR	94.3
5	TRAINING SET DATA	94.1
6	APPROXIMATION ERROR	94.1

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NUMBER OF STUDENTS  
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ADDRESS: \_\_\_\_\_  
CITY: \_\_\_\_\_ STATE: \_\_\_\_\_  
COUNTY: \_\_\_\_\_

SHALLOTT, L. A., and J. A. HARRIS. 1974. The  
OCCURRENCE OF THE COMMON BOTTLE  
NECKED SNAIL IN THE VERMONT AREA.



CURRENT APPLICATION DATA  
1 APPLICATION NUMBER: 177907472078  
2 INFORMATION FOR SEQ ID NO: 1  
3 SEQUENCE CHARACTERISTICS  
4 LENGTH: 192  
5 TYPE: amino acid  
6 TOP LOGIC: 110000  
7 PRT US9412874319

Query Match: 100.00% Score: 25.00 E-01  
Post Local Similarity: 100.00% Prod. No. 10000  
Matches: 72 Conserved: 100% Mismatch: 0% Gaps: 0%

1 101163 5  
2 101163 101163  
3 101163 101163 125

RESULT 12

1 US 09 149 1016 19  
2 Sequence ID: Application US/09/149 1016  
3 Patent No. 6171924  
4 GENERAL INFORMATION:  
5 APPLICANT: Lott, David M.  
6 APPLICANT: Lott, David M.  
7 TITLE OF INVENTION: INJECTED EYE KINES  
8 NUMBER OF SEQUENCES: 20  
9 CORRESPONDENCE ADDRESS:  
10 ADDRESS: Cell Therapeutics, Inc.  
11 STREET: 200 Elliott Avenue West, Suite 600  
12 CITY: Seattle  
13 STATE: Washington  
14 COUNTRY: U.S.A.  
15 ZIP: 98119  
16 COMPUTER REVENUE FORM:  
17 MEDICAL TYPE: 4.50 disk, 1.44MB, dated 10/1/94  
18 COMPUTER: AST IBM compatible  
19 OPERATING SYSTEM: MS DOS Version 6  
20 SOFTWARE: Word for Windows  
21 CURRENT APPLICATION DATA:  
22 APPLICATION NUMBER: US/09/149 1016  
23 FILING DATE: 27-01-1994  
24 ALTERNATIVE: 18-01-1994  
25 NAME: (S) Lott, David M. and (S) Lott, David M.  
26 REGISTRATION NUMBER: 42,590 and 66,111, registered by  
27 REFERENCE/SEQ ID NO: 0100A  
28 REFERENCE/SEQ ID NO: 0100B  
29 TELEPHONE: (206) 264-7100  
30 TELEFAX: (206) 264-6296  
31 INFORMATION FOR SEQ ID NO: 1  
32 SEQUENCE CHARACTERISTICS  
33 LENGTH: 192  
34 TYPE: amino acid  
35 MOLECULE TYPE: Peptide  
36 HYDROPHILIC: 00  
37 ANTI-SENSE: 00  
38 FRAGMENT TYPE:  
39 ORIGINAL SOURCE:  
40 ORGANISM: Homo Sapien  
41 US 09 149 1016 19

Query Match: 100.00% Score: 25.00 E-01  
Post Local Similarity: 100.00% Prod. No. 10000  
Matches: 72 Conserved: 100% Mismatch: 0% Gaps: 0%

1 101163 5  
2 101163 101163  
3 101163 101163 125

RESULT 13  
1 US 09 149 1016 19  
2 Sequence ID: Application US/09/149 1016  
3 Patent No. 6171924  
4 GENERAL INFORMATION:  
5 APPLICANT: Lott, David M.  
6 APPLICANT: Lott, David M.  
7 TITLE OF INVENTION: INJECTED EYE KINES  
8 NUMBER OF SEQUENCES: 20  
9 CORRESPONDENCE ADDRESS:  
10 ADDRESS: Cell Therapeutics, Inc.  
11 STREET: 200 Elliott Avenue West, Suite 600  
12 CITY: Seattle  
13 STATE: Washington  
14 COUNTRY: U.S.A.  
15 ZIP: 98119  
16 COMPUTER REVENUE FORM:  
17 MEDICAL TYPE: 4.50 disk, 1.44MB, dated 10/1/94  
18 COMPUTER: AST IBM compatible  
19 OPERATING SYSTEM: MS DOS Version 6  
20 SOFTWARE: Word for Windows  
21 CURRENT APPLICATION DATA:  
22 APPLICATION NUMBER: US/09/149 1016  
23 FILING DATE: 27-01-1994  
24 ALTERNATIVE: 18-01-1994  
25 NAME: (S) Lott, David M. and (S) Lott, David M.  
26 REGISTRATION NUMBER: 42,590 and 66,111, registered by  
27 REFERENCE/SEQ ID NO: 0100A  
28 REFERENCE/SEQ ID NO: 0100B  
29 TELEPHONE: (206) 264-7100  
30 TELEFAX: (206) 264-6296  
31 INFORMATION FOR SEQ ID NO: 1  
32 SEQUENCE CHARACTERISTICS  
33 LENGTH: 192  
34 TYPE: amino acid  
35 MOLECULE TYPE: Peptide  
36 HYDROPHILIC: 00  
37 ANTI-SENSE: 00  
38 FRAGMENT TYPE:  
39 ORIGINAL SOURCE:  
40 ORGANISM: Homo Sapien  
41 US 09 149 1016 19

Query Match: 100.00% Score: 25.00 E-01  
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1 101163 5  
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3 101163 101163 125

RESULT 14  
1 US 09 149 1016 19  
2 Sequence ID: Application US/09/149 1016  
3 Patent No. 6171924  
4 GENERAL INFORMATION:  
5 APPLICANT: Lott, David M.  
6 APPLICANT: Lott, David M.  
7 TITLE OF INVENTION: INJECTED EYE KINES  
8 NUMBER OF SEQUENCES: 20  
9 CORRESPONDENCE ADDRESS:  
10 ADDRESS: Cell Therapeutics, Inc.  
11 STREET: 200 Elliott Avenue West, Suite 600  
12 CITY: Seattle  
13 STATE: Washington  
14 COUNTRY: U.S.A.  
15 ZIP: 98119  
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20 SOFTWARE: Word for Windows  
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24 ALTERNATIVE: 18-01-1994  
25 NAME: (S) Lott, David M. and (S) Lott, David M.  
26 REGISTRATION NUMBER: 42,590 and 66,111, registered by  
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31 INFORMATION FOR SEQ ID NO: 1  
32 SEQUENCE CHARACTERISTICS  
33 LENGTH: 192  
34 TYPE: amino acid  
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36 HYDROPHILIC: 00  
37 ANTI-SENSE: 00  
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40 ORGANISM: Homo Sapien  
41 US 09 149 1016 19

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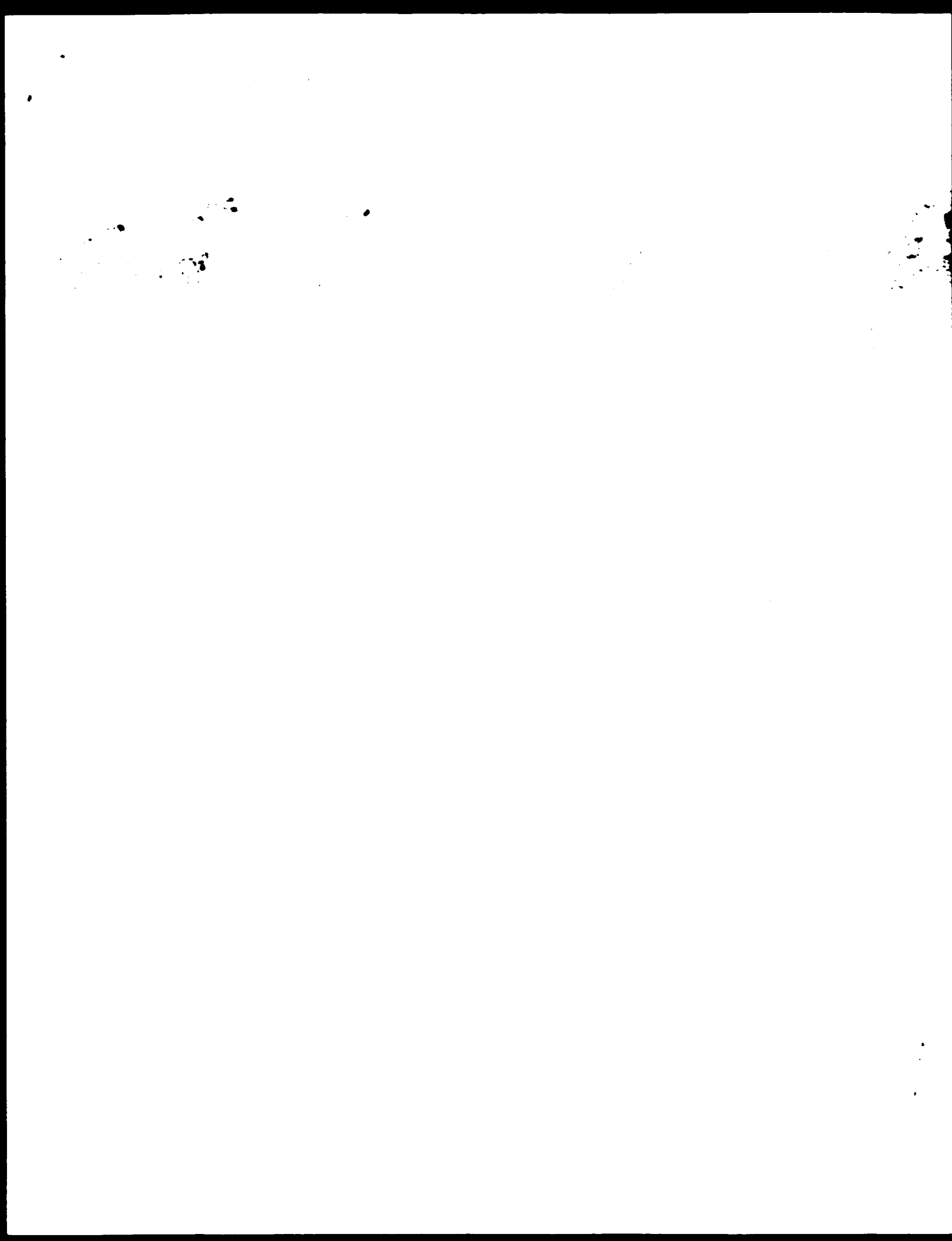




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Page 7





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Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the intervention group (IG). The CG received a standard care (SC) program, while the IG received a SC program plus a cognitive-behavioral intervention (CBI). The CBI was delivered by a trained therapist (T) and consisted of a series of sessions (S) aimed at improving the patient's cognitive and behavioral patterns. The CBI was delivered in a group setting (G) and lasted for 12 weeks (W). The SC program was delivered by a trained therapist (T) and consisted of a series of sessions (S) aimed at providing the patient with information and support. The SC program was delivered in a group setting (G) and lasted for 12 weeks (W). The subjects were followed up for 12 weeks (W) after the end of the intervention. The subjects were assessed at baseline (B) and at follow-up (F). The subjects were assessed using a series of questionnaires (Q) and a clinical interview (I). The subjects were assessed using a series of questionnaires (Q) and a clinical interview (I). The subjects were assessed using a series of questionnaires (Q) and a clinical interview (I).

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Local Control, Stability, and  
Methodology, *Journal of Economic  
Mathematics & Organization*, 34, 1-20

1. *Chlorophyll a* and *Chlorophyll b* were determined using a spectrophotometer (Shimadzu UV-1601) at 663 nm and 646 nm, respectively. The concentration of chlorophyll was calculated using the following formula:  $\text{Chlorophyll } a = 11.8 \times \text{OD}_{663} - 1.8 \times \text{OD}_{646}$  and  $\text{Chlorophyll } b = 21.5 \times \text{OD}_{646} - 5.1 \times \text{OD}_{663}$ . The total chlorophyll concentration was calculated as the sum of chlorophyll *a* and chlorophyll *b*. The concentration of chlorophyll was expressed as  $\mu\text{g mL}^{-1}$ .

1. *Chlorophyll a* and *Chlorophyll b* were determined by the method of Lichtenthaler and Whistler (1973). Total chlorophyll was determined by the method of Arar and Cook (1977). The concentration of chlorophyll was expressed as  $\mu\text{g mL}^{-1}$  of the culture medium.

**TABLE 1** *Summary of the data sets used in the study*

Dataset	Number of subjects	Number of trials	Number of conditions	Number of trials per condition
Experiment 1	10	100	10	10
Experiment 2	10	100	10	10
Experiment 3	10	100	10	10
Experiment 4	10	100	10	10
Experiment 5	10	100	10	10
Experiment 6	10	100	10	10
Experiment 7	10	100	10	10
Experiment 8	10	100	10	10
Experiment 9	10	100	10	10
Experiment 10	10	100	10	10













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DR	InterPro: IPR01679; DNA_14450_N.
DR	InterPro: IPR00445; HHH.

**THEOREM 1.** Let  $(\Omega, \mathcal{F}, P)$  be a probability space and let  $\{X_t\}_{t \geq 0}$  be a stochastic process adapted to a filtration  $\{\mathcal{F}_t\}_{t \geq 0}$ . Suppose that  $X_0 = x$  and that  $X_t$  satisfies the SDE













FIGURE: NMR020201  
 KINASE: TRANSFERASE: COMPLETE PROTEOMES  
 SEQUENCE: 172 AA: 19936 MW: 24936.962112

Query Match  
 Host Local Similarity: 100.00% (Protein No. 24936.962112)

Matches: 52 Conservative: 00% Mismatches: 00% Indels: 00%

QY 1 11111  
 DE 92 11111 96

RESULT 12  
 QY06P5

AC QY06P5 PRELIMINARY: PRT: 183 AA

DI 01-001-2000 (Tribble et al., 1995, last sequence)

DI 01-001-2000 (Tribble et al., 1995, last sequence)

DI 01-001-2000 (Tribble et al., 1995, last sequence)

DE YEAST BETA-100000 INVOLVED IN TACETIN AND STONER TO 0.001

DE TRANSFER VESTIGES: HYDROPHILIC PROTEIN HAT WITH INHIBITION WITH

DE SNARE PROTEINS

DE SPACED 1st

OS Schizosaccharomyces pombe (Yeast)

OS Eukaryotic Protein: Ascomycota: Schizosaccharomyces pombe

OS Schizosaccharomyces pombe: Schizosaccharomyces pombe

OS NMR: 14111 4896

QX NMR: 14111 4896

QY NMR: 14111 4896

QZ NMR: 14111 4896

QY NMR: 14111 4896

QZ NMR: 14111 4896

QY NMR: 14111 4896

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FIGURE: NMR020201  
 KINASE: TRANSFERASE: COMPLETE PROTEOMES  
 SEQUENCE: 172 AA: 19936 MW: 24936.962112

Query Match  
 Host Local Similarity: 100.00% (Protein No. 24936.962112)

QY 1 11111  
 DE 92 11111 96

RESULT 13  
 QY06P5

AC QY06P5 PRELIMINARY: PRT: 183 AA

DI 01-001-2000 (Tribble et al., 1995, last sequence)

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QX NMR: 14111 4896

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